1. Main bacterial phyla: ***Bacteroidetes, Firmicutes, Proteobacteria, Fusobacteria, Actinobacteria*** (Fan et al., 2018) .

Reference：Fan X, Peters BA, Min D, Ahn J, Hayes RB. 2018. Comparison of the oral microbiome in mouthwash and whole saliva samples. Public library of science one 13(4): e194729.  [DOI 10.1371/journal.pone.0194729](https://doi.org/10.1371/journal.pone.0194729)

1. The 10 most abundant genera: ***Streptococcus, Prevotella, Porphyromonas, Neisseria, Veillonella, Granulicatella, Actinomyces, Haemophilus, Rothia, Fusobacterium*.** (Omori et al., 2021).

Reference：Omori M, Kato-Kogoe N, Sakaguchi S, Fukui N, Yamamoto K, Nakajima Y, Inoue K, Nakano H, Motooka D, Nakano T, Nakamura S, Ueno T. 2021. Comparative evaluation of microbial profiles of oral samples obtained at different collection time points and using different methods. *Clinical Oral Investigations* 25(5): 2779-2789.  [DOI 10.1007/s00784-020-03592-y](https://doi.org/10.1007/s00784-020-03592-y)

***3.Streptococcus*** genus is most abundant in unstimulated saliva samples (Gomar Vercher et al., 2018) .

Reference：**：**Gomar-Vercher, S., Simón-Soro, A., Montiel-Company, J. M., Almerich-Silla, J. M., and Mira, A. (2018). Stimulated and unstimulated saliva samples have significantly different bacterial profiles. PLoS One 13, e0198021. DOI: 10.1371/journal.pone.0198021

4.Oral bacterial spectrum similar to saliva samples obtained by spitting method (Fan et al., 2018).

Reference：Fan X, Peters BA, Min D, Ahn J, Hayes RB. 2018. Comparison of the oral microbiome in mouthwash and whole saliva samples. *Public library of science one* 13(4): e194729.  [DOI 10.1371/journal.pone.0194729](https://doi.org/10.1371/journal.pone.0194729)

1. The microorganisms in the saliva collected by Scope mouthwash are usually stable. After being stored at room temperature for 4 days, the abundance of ***Firmicutes*** increases, while the abundance of ***Proteobacteria***decreases (Wu et al., 2021).

Reference：Wu Z, Hullings AG, Ghanbari R, Etemadi A, Wan Y, Zhu B, Poustchi H, Fahraji BB, Sakhvidi MJZ, Shi J, Knight R, Malekzadeh R, Sinha R, Vogtmann E. 2021. Comparison of fecal and oral collection methods for studies of the human microbiota in two Iranian cohorts. *Bmc Microbiology* 21(1): 324.  [DOI 10.1186/s12866-021-02387-9](https://doi.org/10.1186/s12866-021-02387-9)

1. At the genus level, ***Streptococcus***occupies 20–35% of the total sequences in stimulated saliva, followed by ***Neisseria***(7–25%), ***Prevotella***(2–25%) and ***Veillonella*** (6–22%) , ***Fusobacterium***(＜10%) and ***Porphyromonas*** (7%). ***Fusobacterium***and ***Porphyromonas***were two typical inhabitants of dental plaque. ***Streptococcus*** is the most abundant in the unstimulated saliva samples, many other bacterial genera are either at low proportion or absent when compared with stimulated saliva (Gomar Vercher et al., 2018).

Reference：Gomar-Vercher, S., Simón-Soro, A., Montiel-Company, J. M., Almerich-Silla, J. M., and Mira, A. (2018). Stimulated and unstimulated saliva samples have significantly different bacterial profiles. PLoS One 13, e0198021. DOI: 10.1371/journal.pone.0198021

7.Similar composition of salivary microbiota between olfactory stimulation and passive drooling. (Zhu et al., 2020).

Reference：Zhu, C., Yuan, C., Wei, F. Q., Sun, X. Y., and Zheng, S. G. (2020). Comparative evaluation of peptidome and microbiota in different types of saliva samples. Ann. Transl. Med. 8, 686. DOI: 10.21037/atm-20-393

8.Compared to unstimulated saliva, taste stimulation can lead to significant changes in the microbiota (Zhu et al., 2020).

Reference：Zhu, C., Yuan, C., Wei, F. Q., Sun, X. Y., and Zheng, S. G. (2020). Comparative evaluation of peptidome and microbiota in different types of saliva samples. Ann. Transl. Med. 8, 686. DOI: 10.21037/atm-20-393

9.The cotton swab method and the spitting method gave significantly different results. The oral swab method tends to contain less ***Prevotella*** and more ***Haemophilus*** at the genus level (Omori et al., 2021).

Reference：Omori M, Kato-Kogoe N, Sakaguchi S, Fukui N, Yamamoto K, Nakajima Y, Inoue K, Nakano H, Motooka D, Nakano T, Nakamura S, Ueno T. 2021. Comparative evaluation of microbial profiles of oral samples obtained at different collection time points and using different methods. *Clinical Oral Investigations* 25(5): 2779-2789.  [DOI 10.1007/s00784-020-03592-y](https://doi.org/10.1007/s00784-020-03592-y)

1. Phyla pattern was similar between swabs and tissues. Main phyla: ***Firmicutes****,* ***Proteobacteria****,* ***Bacteroidetes****,* ***Actinobacteria***. In 2 month old mice, *Cutibacterium acnes* was detected in higher abundance in the tissue biopsies. (Hernández Arriaga et al., 2019).

Reference：Hernández-Arriaga A, Baumann A, Witte OW, Frahm C, Bergheim I, Camarinha-Silva A. 2019. Changes in Oral Microbial Ecology of C57BL/6 Mice at Different Ages Associated with Sampling Methodology. Microorganisms 7(9). [DOI 10.3390/microorganisms7090283](https://doi.org/10.3390/microorganisms7090283)

1. Phyla pattern was similar between swabs and tissues. Main phyla: ***Firmicutes, Proteobacteria, Bacteroidetes, Actinobacteria***.In 15 month old animals, *Corynebacterium* was more abundant in the swabs. In 2 month old mice, *Streptococcus* danieliae was more abundant in swab.(Hernández Arriaga et al., 2019).

Reference: Hernández-Arriaga A, Baumann A, Witte OW, Frahm C, Bergheim I, Camarinha-Silva A. 2019. Changes in Oral Microbial Ecology of C57BL/6 Mice at Different Ages Associated with Sampling Methodology. Microorganisms 7(9). [DOI 10.3390/microorganisms7090283](https://doi.org/10.3390/microorganisms7090283)

12.The average bacterial counts and the numbers of A.actinomycetemcomitans obtained by the paper point or the curette sampling method did not show signiﬁcant diﬀerence. Aggregatibacter actinomycetemcomitans 56%(36% positive and 20% negative) , Porphyromonas gingivalis 96%(88% positive and 8% negative), Treponema denticola98%(94% positive and 4% negative), Tannerella forsythia 96%(96% positive and 0% negative). Frequency of detecting targeted taxa using curette: Aggregatibacter actinomycetemcomitans 14%, Porphyromonas gingivalis 4%, Tannerella forsythia 2%, Treponema denticola 0%. (Belibasakis et al., 2013)

Reference：Belibasakis, G. N., Schmidlin, P. R., and Sahrmann, P. (2013). Molecular microbiological evaluation of subgingival biofilm sampling by paper point and curette. APMIS 122, 347-52. DOI: 10.1111/apm.12151

13.The Frequency of detecting targeted taxa using paper points: Aggregatibacter actinomycetemcomitans 30%,Treponema denticola2%, Tannerella forsythia 2%, Porphyromonas gingivalis 0%. Compared with the curette, the paper point detected significantly higher levels of the three "red complexes". Paper point can more consistently detect the presence of A. actinomycetemcomitans in patients with invasive periodontitis than the curette method. (Belibasakis et al., 2013)

Reference：Belibasakis, G. N., Schmidlin, P. R., and Sahrmann, P. (2013). Molecular microbiological evaluation of subgingival biofilm sampling by paper point and curette. APMIS 122, 347-52. DOI: 10.1111/apm.12151

14.(Normal, Esophagitis, LGIN, HGIN, ESCC) The top 5 bacterial phyla:***Firmicutes****,* ***Proteobacteria****,* ***Bacteroidetes****,* ***Actinobacteria****,* ***Fusobacteria****.* The top 10 genera: ***Streptococcus***,***Prevotella***,***Veillonella***, ***Actinobacillus***,***Haemophilus***, ***Neisseria****,* ***Alloprevotella****,* ***Rothia****,* ***Gemella****,* ***Porphyromonas***. (Li et al., 2020).

Reference：Li M, Shao D, Zhou J, Gu J, Qin J, Chen W, Wei W. 2020. Signatures within esophageal microbiota with progression of esophageal squamous cell carcinoma. Chinese Journal of Cancer Research 32(6): 755-767. [DOI 10.21147/j.issn.1000-9604.2020.06.09](https://doi.org/10.21147/j.issn.1000-9604.2020.06.09)

15.(The carcinoma and adjacent normal tissue) phylum level: ***Bacteroidetes*, *Firmicutes*, *Proteobacteria*, *Fusobacteria, Actinobacteria****;* top ten genera: ***Prevotella, Streptococcus, Veillonella, [Prevotella], Haemophilus****,* ***Capnocytophaga, Fusobacterium, Selenomonas, Peptostreptococcus, Neisseria****. (Liu et al., 2019).*

Reference：Liu, A. Q., Vogtmann, E., Shao, D. T., Abnet, C. C., Dou, H. Y., Qin, Y., et al. (2019). A comparison of biopsy and mucosal swab specimens for examining the microbiota of upper gastrointestinal carcinoma. Cancer Epidemiol. Biomarkers Prev. 28, 2030-2037.DOI: 10.1158/1055-9965.EPI-18-1210

16.The endoscopic brush consistently has all of the OTUs found in the biopsy samples, as well as additional OTUs. In the Barrett esophagus cohort, *Streptococcus* and *Prevotella* are dominant in the upper gastrointestinal tract. (Gall rt al., 2015)

Reference：Gall, A., Fero, J., McCoy, C., Claywell, B. C., Sanchez, C. A., Blount, P. L., et al. (2015). Bacterial composition of the human upper gastrointestinal tract microbiome is dynamic and associated with genomic instability in a barrett's esophagus cohort. PLoS One 10, e0129055. DOI: 10.1371/journal.pone.0129055

17.The swab mucosa and tissue biopsy specimens have similar microbial profile (Li et al., 2020; Liu et al., 2019).

References：

Li M, Shao D, Zhou J, Gu J, Qin J, Chen W, Wei W. 2020. Signatures within esophageal microbiota with progression of esophageal squamous cell carcinoma. Chinese Journal of Cancer Research 32(6): 755-767. [DOI 10.21147/j.issn.1000-9604.2020.06.09](https://doi.org/10.21147/j.issn.1000-9604.2020.06.09)

Liu, A. Q., Vogtmann, E., Shao, D. T., Abnet, C. C., Dou, H. Y., Qin, Y., et al. (2019). A comparison of biopsy and mucosal swab specimens for examining the microbiota of upper gastrointestinal carcinoma. Cancer Epidemiol. Biomarkers Prev. 28, 2030-2037. DOI: 10.1158/1055-9965.EPI-18-1210

18.There is a difference in the structure of esophageal microbial communities between tissue samples and liquid samples. In esophageal fluid ***Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria, Fusobacteria***were the dominant phyla, ***Streptococcus, Prevotella, Veillonella, Gemella, Rothia, Haemophilu***with higher abundance ratios at the genus level. (Jung et al., 2022).

Reference：Jung DH, Youn YH, Kim DH, Lim CH, Lim HS, Moon HS, Lee JY, Park H, Hong SJ. 2022. Esophageal microbiota and nutritional intakes in patients with achalasia before and after peroral endoscopic myotomy. Journal of Neurogastroenterology and Motility 28(2): 237-246.  [DOI: 10.5056/jnm21057](https://doi.org/10.5056/jnm21057)

19.(healthy, Barrett's oesophagus, esophageal adenocarcinoma) The eight most prevalent phyla: ***Bacteroidetes, Proteobacteria, Fusobacteria, Actinobacteria, Spirochaetes,* SR1, TM7**. representative genera: ***Veillonella, Dialister, Selenomonas, Megasphaera, Granulicatella, Oribacterium, Catonella, Moryella, Solobacterium, Campylobacter, Olsenella, Atopobium, Actinomyces*** (Elliott et al., 2016).

Reference：Elliott DRF, Walker AW, O'Donovan M, Parkhill J, Fitzgerald RC. 2017.A non-endoscopic device to sample the oesophageal microbiota: a case-control study. *The lancet Gastroenterology & hepatology* 2(1): 32-42.  [DOI 10.1016/S2468-1253(16)30086-3](https://doi.org/10.1016/S2468-1253(16)30086-3)

20.The microbiota of esophageal biopsy and EST are almost the same. the relative abundance of the main bacterial phyla (***Actinobacteria, Bacteroidetes, Firmicutes, Fusobacteria, Proteobacteria***) is similar. The overlap percentage of common bacterial genera is higher than 75%, and the number of genera in biopsy is higher than that in ESTs(Fillon et al., 2012).

Reference：Fillon SA, Harris JK, Wagner BD, Kelly CJ, Stevens MJ, Moore W, Fang R, Schroeder S, Masterson JC, Robertson CE, Pace NR, Ackerman SJ, Furuta GT. 2012. Novel device to sample the esophageal microbiome--the esophageal string test. *Public library of science one* 7(9): e42938.  [DOI 10.1371/journal.pone.0042938](https://doi.org/10.1371/journal.pone.0042938)

21.At the phylum level, normal gastric mucosa: ***Proteobacteria, Firmicutes, Bacteroidetes, Actinobacteria, Verrucomicrobia*, *Cyanobacteria***; equine glandular gastric disease lesion: ***Firmicutes, Proteobacteria, Bacteroidetes, Verrucomicrobia, Actinobacteria, Cyanobacteria*** (Voss et al., 2022).

Reference：Voss SJ, McGuinness DH, Weir W, Sutton DGM. 2022. A study comparing the healthy and diseased equine glandular gastric microbiota sampled with sheathed transendoscopic cytology brushes. *Journal of Equine Veterinary Science* 116: 104002. [DOI 10.1016/j.jevs.2022.104002](https://doi.org/10.1016/j.jevs.2022.104002)

22.The sensitivity of biopsy forceps scraping mucosal rapid urease test was higher than that of tissue biopsy, PCR sensitivity was higher than that of standard biopsy, specificity (99.5%) and overall accuracy (95.3%) were higher than that of standard biopsy samples and gastric juice (Matsumoto et al., 2016).

Reference：Matsumoto H, Kuroki Y, Higashi S, Goda K, Fukushima S, Katsumoto R, Oosawa M, Murao T, Ishii M, Oka K, Takahashi M, Osaki T, Kamiya S, Shiotani A. 2019.Analysis of the colonic mucosa associated microbiota (MAM) using brushing samples during colonic endoscopic procedures. *Journal of Clinical Biochemistry Nutrition* 65(2): 132-137. [DOI 10.3164/jcbn.19-3](https://doi.org/10.3164/jcbn.19-3)

23.The recovery rate of *Helicobacter pylori* was 100% after storing for 24 h and 72 h before culture (Graham et al. , 2005)

Reference：Graham DY, Kudo M, Reddy R, Opekun AR. 2005. Practical rapid, minimally invasive, reliable nonendoscopic method to obtain Helicobacter pylori for culture. *Helicobacter* 10(1): 1-3.  [DOI 10.1111/j.1523-5378.2005.00285.x](https://doi.org/10.1111/j.1523-5378.2005.00285.x)

24.At the phylum level, control: ***Firmicutes,* Non-Hp *proteobacteria, Bacteroidetes, Actinobacteria, Fusobacteria***; gastritis: ***H. pylori,* Non-Hp *proteobacteria***; early gastric cancer: ***H. pylori,* Non-Hp *proteobacteria, Firmicutes***; advanced gastric cancer: ***H. pylori, Firmicutes,* Non-Hp *proteobacteria, Bacteroidetes, Fusobacteria, Actinobacteria*** (Sung et al., 2016).

Reference：Sung J, Kim N, Kim J, Jo HJ, Park JH, Nam RH, Seok YJ, Kim YR, Lee DH, Jung HC. 2016.Comparison of gastric microbiota between gastric juice and mucosa by next generation sequencing method. *Journal of cancer prevention* 21(1): 60-65.  [DOI 10.15430/JCP.2016.21.1.60](https://doi.org/10.15430/JCP.2016.21.1.60)

25.At the phylum level, the control: ***Actinobacteria,* Non- *H.pylori proteobacteria, Firmicutes, Bacteroidetes***; gastritis: ***Firmicutes, Actinobacteria, Bacteroidetes,* Non- *H.pylori proteobacteria, Fusobacteria*;** early gastric cancer: ***Firmicutes,* Non- *H.pylori proteobacteria, Bacteroidetes, H. pylori***; advanced gastric cancer: ***Bacteroidetes,* Non-Hp *proteobacteria, Firmicutes, Fusobacteria, H. pylori*.** (Sung et al., 2016) (Matsumoto et al., 2019)

References：

Sung J, Kim N, Kim J, Jo HJ, Park JH, Nam RH, Seok YJ, Kim YR, Lee DH, Jung HC. 2016. Comparison of gastric microbiota between gastric juice and mucosa by next generation sequencing method. *Journal of cancer prevention* 21(1): 60-65. [DOI: 10.15430/JCP.2016.21.1.60](https://doi.org/10.15430/JCP.2016.21.1.60)

Matsumoto H, Kuroki Y, Higashi S, Goda K, Fukushima S, Katsumoto R, Oosawa M, Murao T, Ishii M, Oka K, Takahashi M, Osaki T, Kamiya S, Shiotani A. 2019.Analysis of the colonic mucosa associated microbiota (MAM) using brushing samples during colonic endoscopic procedures. *Journal of Clinical Biochemistry Nutrition* 65(2): 132-137. [DOI: 10.3164/jcbn.19-3](https://doi.org/10.3164/jcbn.19-3)

26.Compared with the 13C urea breath test, the diagnostic rate of ***H.pylori*** infection using string-­test qPCR was 95.9%, 93.6% positive, and 100% negative.The eradication rate of ***H.pylori*** infection under the guidance of drug sensitivity in string-­test sample culture was 91.8%, which is higher than empirical treatment (81.3%) (Han et al., 2023).

Reference：Han X, Yu X, Gao X, Wang X, Tay CY, Wei X, Lai B, Marshall BJ, Zhang X, Chua EG. 2023. Quantitative PCR of string-test collected gastric material: A feasible approach to detect Helicobacter pylori and its resistance against clarithromycin and levofloxacin for susceptibility-guided therapy. *Helicobacter* 28(4): e12985.  [DOI 10.1111/hel.12985](https://doi.org/10.1111/hel.12985)

27.Main phyla: ***Firmicutes*** (>50%), ***Proteobacteria, Actinobacteria, Fusobacteria, Bacteroidetes, TM7****.* ***Firmicutes*** are mainly ***Lactobacillus***, including ***Streptococcus, Lactobacillu****s* and ***Botulinum***. ***Proteobacteria*** are mainly represented by ***Neisseria, Pasteurellaceae*** and ***Enterobacteriaceae*** (Leite et al. , 2020).

Reference：Leite GGS, Weitsman S, Parodi G, Celly S, Sedighi R, Sanchez M, Morales W, Villanueva-Millan MJ, Barlow GM, Mathur R, Lo SK, Jamil LH, Paski S, Rezaie A, Pimentel M. 2020. Mapping the segmental microbiomes in the human small bowel in comparison with stool: a relmagine syudy. Digestive diseases and sciences 65(9): 2595-2604. [DOI :10.1007/s10620-020-06173-x](https://doi.org/10.1007/s10620-020-06173-x)28.

28.Main phyla: Firmicutes (>60%), Bacteroidetes, Proteobacteria, Actinobacteria, Fusobacteria, TM7 and Acidobacteria; most abundant genera: Streptococcus, Prevotella, Veillonella, Neisseria, Porphyromonas, Lactobacillus.(Shanahan et al., 2016) .

Reference：Shanahan ER, Zhong L, Talley NJ, Morrison M, Holtmann G. 2016. Characterisation of the gastrointestinal mucosa-associated microbiota: a novel technique to prevent cross-contamination during endoscopic procedures. Alimentary Pharmacology and Therapeutics 43(11): 1186-1196.  [DOI: 10.1111/apt.13622](https://doi.org/10.1111/apt.13622)

29.(ileal pouch) Mucosal brushings and mucosal biopsies provide comparable results for sampling the mucosa-associated microbiota. The ten most abundant taxa : Bacteroides, Lachnospiraceae, Clostridium, Enterobacteriaceae,Blautia,  Roseburia,  Epulopiscium, Peptostreptococcaceae, Acidaminococcus and Streptococcus(Huse et al.,2014).Main phyla: Firmicutes (>60%), Bacteroidetes, Proteobacteria, Actinobacteria, Fusobacteria, TM7 and Acidobacteria; most abundant genera: Streptococcus, Prevotella, Veillonella, Neisseria, Porphyromonas, Lactobacillus (Shanahan et al., 2016).

References：

Huse SM, Young VB, Morrison HG, Antonopoulos DA, Kwon J, Dalal S, Arrieta R, Hubert NA, Shen L, Vineis JH, Koval JC, Sogin ML, Chang EB, Raffals LE. 2014. Comparison of brush and biopsy sampling methods of the ileal pouch for assessment of mucosa-associated microbiota of human subjects. Microbiome 2(1): 5. [DOI 10.1186/2049-2618-2-5](https://doi.org/%2010.1186/2049-2618-2-5)

Shanahan ER, Zhong L, Talley NJ, Morrison M, Holtmann G. 2016. Characterisation of the gastrointestinal mucosa-associated microbiota: a novel technique to prevent cross-contamination during endoscopic procedures. Alimentary Pharmacology and Therapeutics 43(11): 1186-1196.  [DOI:10.1111/apt.13622](https://doi.org/10.1111/apt.13622)

30.The five most abundant phyla: ***Firmicutes, Proteobacteria, Actinobacteria, Bacteroidetes, Fusobacteria***.The most abundant genera are as follows: dodecadactylon (***Veillonella, Streptococcus, Prevotella, Haemophilus, Actinomyces***), jejunum (***Streptococcus, Veillonella, Escherichia, Actinomyces, Haemophilus***), ileum (***Escherichia, Haemophilus, Streptococcus, Bacteroides, Veillonella***), terminal ileum( ***Escherichia, Bacteroides, Haemophilus, Streptococcus, Clostridium* cluster XIVa).** (Nagasue et al.,2022).

Reference：Nagasue T, Hirano A, Torisu T, Umeno J, Shibata H, Moriyama T, Kawasaki K, Fujioka S, Fuyuno Y, Matsuno Y, Esaki M, Kitazono T. 2022.The compositional structure of the small intestinal microbial community via balloon-assisted enteroscopy. *Digestion* 103(4): 308-318.  [DOI 10.1159/000524023](https://doi.org/10.1159/000524023)

31.The most frequent bacteria were ***Streptococcus salivarius/vestibularis, S. parasanguinis, S. mitis/oralis, Rothia mucilaginosa, Actinomyces odontolyticus, Haemophilus parainfluenzae, Neisseria flavescens/subflava***and***Neisseria parahaemolyticus.***(Villmones et al. , 2022).

Reference：Villmones HC, Svanevik M, Ulvestad E, Stenstad T, Anthonisen IL, Nygaard RM, Dyrhovden R, Kommedal Ø. 2022. Investigating the human jejunal microbiota. *Scientific reports* 12(1): 1682.  [DOI 10.1038/s41598-022-05723-9](https://doi.org/10.1038/s41598-022-05723-9)

32.***Bacilli* (*Streptococcus sp.*),*Clostridium*clusters XIVa** (several genera) have a high abundance in the ileostoma effluent.  (Zoetendal et al., 2012)

Reference：Zoetendal EG, Raes J, van den Bogert B, Arumugam M, Booijink CC, Troost FJ, Bork P, Wels M, de Vos WM, Kleerebezem M. 2012. The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. *The ISME journal* 6(7): 1415-1426.  [DOI 10.1038/ismej.2011.212](https://doi.org/10.1038/ismej.2011.212)

33.The main bacterial phyla in the feces of healthy individuals include ***Firmicutes, Bacteroidetes,***and***Proteobacteria*** . (Radhakrishnan et al., 2023).

Reference：Radhakrishnan, S. T., Gallagher, K. I., Mullish, B. H., Serrano-Contreras, J. I., Alexander, J. L., Miguens Blanco, J., et al. (2023). Rectal swabs as a viable alternative to faecal sampling for the analysis of gut microbiota functionality and composition. Sci.Rep. 13, 493. DOI: 10.1038/s41598-022-27131-9

34.At the genus level, stool samples had higher relative abundances of members of the***Akkermansia, Bacteroides, Enterococcus,***and***Parabacteroides* taxa**, which are considered typical members of the gut microbiome in critically ill patients (Fair et al., 2019) .

Reference：Fair, K., Dunlap, D. G., Fitch, A., Bogdanovich, T., Methé, B., Morris, A., et al. (2019). Rectal swabs from critically ill patients provide discordant representations of the gut microbiome compared to stool samples. mSphere 4, e00358-19. DOI: 10.1128/mSphere.00358-19

35.The most common bacterial pathogens in fecal culture include ***Shigella, Salmonella*,** Shiga toxin-producing***E. coli*,** and ***Campylobacter****.* (Jean et al., 2019)

Reference：Jean, S., Yarbrough, M. L., Anderson, N. W., and Burnham, C. A. (2019). Culture of rectal swab specimens for enteric bacterial pathogens decreases time to test result while preserving assay sensitivity compared to bulk fecal specimens. J. Clin. Microbiol. 57, e02077-18. DOI: 10.1128/JCM.02077-18

36.Compared with RNA later samples, the abundance of ***Bacteroidetes*** in fecal samples collected by FOBT cards is significantly lower, but the abundance of ***Actinobacteria*** and ***Firmicutes*** is higher(Wu et al.,2021).

Reference：Wu Z, Hullings AG, Ghanbari R, Etemadi A, Wan Y, Zhu B, Poustchi H, Fahraji BB, Sakhvidi MJZ, Shi J, Knight R, Malekzadeh R, Sinha R, Vogtmann E. 2021.Comparison of fecal and oral collection methods for studies of the human microbiota in two Iranian cohorts. *Bmc Microbiology* 21(1): 324.  [DOI 10.1186/s12866-021-02387-9](https://doi.org/10.1186/s12866-021-02387-9)

37.The swab method has similar microbial community results with feces. the phylum ***Proteobacteria*** and the genus***WAL-1855D*** (a Sporobacterium) is enriched in swab samples. (Short et al., 2021)

Reference：Short, M. I., Hudson, R., Besasie, B. D., Reveles, K. R., Shah, D. P., Nicholson, S., et al. (2021). Comparison of rectal swab, glove tip, and participant-collected stool techniques for gut microbiome sampling. BMC Microbiol. 21, 26. DOI: 10.1186/s12866-020-02080-3

38.Glove-tip collection is similar to swab collection techniques and is often similar to household fecal collection. ***Oscillospira*** is enriched in glove tip samples. (Short et al., 2021)

Reference：Short, M. I., Hudson, R., Besasie, B. D., Reveles, K. R., Shah, D. P., Nicholson, S., et al. (2021). Comparison of rectal swab, glove tip, and participant-collected stool techniques for gut microbiome sampling. BMC Microbiol. 21, 26. DOI: 10.1186/s12866-020-02080-3

39.The main members of the gut microbiota include ***Clostridium spp, Bifidobacterium spp, Bacteroides spp, Lactobacillus spp*** and***E. coli****.* (AraújoPérez et al., 2012)

Reference：Araújo-Pérez F, McCoy AN, Okechukwu C, Carroll IM, Smith KM, Jeremiah K, Sandler RS, Asher GN, Keku TO. 2012. Differences in microbial signatures between rectal mucosal biopsies and rectal swabs. *Gut microbes* 3(6): 530-535. [DOI 10.4161/gmic.22157](https://doi.org/10.4161/gmic.22157)

40..At the phylum level, the abundance of ***Actinobacteria*** is more abundant at the endoscopic brush sample level, while the abundance of ***Bacteroidetes*** is less rich. In the class levels, ***Actinobacteria* (*Bifidobacteriale*)** and ***Bacilli* (*Lactobacillales*)** tended to be richer in brushing samples, while ***Bacteroidia (Bacteroides)*** is less rich. At the genus level, the abundance ***Veillonella, Bulleidia*** and ***Corynebacterium*** in the ascending colon and ***Lactobacillus***and ***Corynebacterium***in the sigmoid colon significantly increased in brushing samples (Matsumoto et al., 2019).

Reference：Matsumoto H, Kuroki Y, Higashi S, Goda K, Fukushima S, Katsumoto R, Oosawa M, Murao T, Ishii M, Oka K, Takahashi M, Osaki T, Kamiya S, Shiotani A. 2019. Analysis of the colonic mucosa associated microbiota (MAM) using brushing samples during colonic endoscopic procedures. *Journal of Clinical Biochemistry Nutrition* 65(2): 132-137. [DOI 10.3164/jcbn.19-3](https://doi.org/10.3164/jcbn.19-3).

1. The dominant bacteria in the lavage samples were ***Firmicutes, Bacteroidetes, Proteobacteria, Actinomycetes*** (Watt et al. , 2016) .The main bacterial phyla ***Firmicutes, Bacteroides, Proteobacteria, Actinobacteria, Fusobacteria*.** (Kwon et al. , 2021)

Reference：Kwon, Y. J., Kwak, H. J., Lee, H. K., Lim, H. C., and Jung, D. H. (2021). Comparison of bacterial community profiles from large intestine specimens, rectal swabs, and stool samples. Appl. Microbiol. Biotechnol. 105, 9273-9284. DOI: 10.1007/s00253-021-11650-y

42.The most dominant phyla were ***Proteobacteria*** (61.7%) , ***Firmicutes*** (25.1%) , ***Bacteroidetes*** (5%) , ***Fusobacteria*** (4.6%) and ***Actinomycetes***(2.6%) .The content of ***Enterococcus*** in bile of patients with brown pigment stone was rich (Kim et al. , 2021). ***Bacteroides fragilis*** is significantly associated with cholangitis (Effenberger et al. , 2023).

Reference：Effenberger M, Al-Zoairy R, Gstir R, Graziadei I, Schwaighofer H, Tilg H, Zoller H. 2023. Transmission of oral microbiota to the biliary tract during endoscopic retrograde cholangiography. Bmc Gastroenterology 23(1): 103.  [DOI 10.1186/s12876-023-02721-7](https://doi.org/10.1186/s12876-023-02721-7)

43.The main bacterial phyla of bile include Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria. In patients with cholelithiasis members of the families Bacteroidaceae, Prevotellaceae, Porphyromonadaceae, Veillonellaceae were more frequently detected. (Molinero et al., 2019)

Reference：Molinero N, Ruiz L, Milani C, Gutiérrez-Díaz I, Sánchez B, Mangifesta M, Segura J, Cambero I, Campelo AB, García-Bernardo CM, Cabrera A, Rodríguez JI, González S, Rodríguez JM, Ventura M, Delgado S, Margolles A. 2019. The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. Microbiome 7(1): 100. [DOI 10.1186/s40168-019-0712-8](https://doi.org/10.1186/s40168-019-0712-8)

44.Dominant phylum: ***Proteobacteria、Firmicutes、Actinobacteriota, Bacteroidota*.** Dominant genera: ***Aliidiomarina, Halomonas, Dietzia,*** and ***Achromobacter.*** At the phylum level, ***Actinobacteriota***and ***Verrucomicrobiota*** genera had significantly lower abundance in HCC tissues than in paraneoplastic tissue. At the genus level, the abundances of the genera***Dietzia, Faecalibacterium, Megamonas, Hydrogenophaga, Agathobacter, Chryseobacterium,*** and***Ruminococcaceae*** were significantly lower, while the abundances of ***Neisseria, Clostridia\_UCG-014,******Fusobacterium***, and ***Lactobacillus*** were significantly higher in HCC tissues than in paracancerous Tissues (He et al., 2023).

Reference：He Y, Zhang Q, Yu X, Zhang S, Guo W. 2023. Overview of microbial profiles in human hepatocellular carcinoma and adjacent nontumor tissues. Journal of Translational Medicine 21(1): 68.  [DOI 10.1186/s12967-023-03938-6](https://doi.org/10.1186/s12967-023-03938-6) References：He Y, Zhang Q, Yu X, Zhang S, Guo W. 2023. Overview of microbial profiles in human hepatocellular carcinoma and adjacent nontumor tissues. Journal of Translational Medicine 21(1): 68. [DOI 10.1186/s12967-023-03938-6](https://doi.org/10.1186/s12967-023-03938-6)

45.Bacteria with high abundance included ***Burkholderiales, Pseudomonadales,******Xanthomonadales, Bacillales, Clostridiales*,** and ***Sphingomonadales*.** Using the bacterial culture experiments, ***Staphylococcus*** capitis in fresh tumor tissue of ICC was found (Chai et al., 2023).

Reference:Chai, X., Wang, J., Li, H., Gao, C., Li, S., Wei, C., et al. (2023). Intratumor microbiome features reveal antitumor potentials of intrahepatic cholangiocarcinoma. Gut Microbes 15, 2156255. DOI: 10.1080/19490976.2022.2156255

46..Major bacterial phyla: ***Proteobacteria*** (45.9%) , ***Firmicutes*** (35.6%) , ***Bacteroidetes*** (9.5%) , ***Fusobacteria*** (4.3%) , and ***Actinomycetes*** (3.9%) (Del Castillo et al. , 2020).

Reference：Del Castillo E, Meier R, Chung M, Koestler DC, Chen T, Paster BJ, Charpentier KP, Kelsey KT, Izard J, Michaud DS. 2019. The microbiomes of pancreatic and duodenum tissue overlap and are highly subject specific but differ between pancreatic cancer and noncancer subjects. Cancer epidemiology, biomarkers & prevention 28(2): 370-383. [DOI 10.1158/1055-9965.EPI-18-0542](https://doi.org/10.1158/1055-9965.EPI-18-0542)

47.Main bacterial phylum: Proteobacteria, Firmicutes, Bacteroidetes, Actinobacteria, Fusobacteria. There was no significant difference in tumor bacterial diversity and composition at the bacterial phylum level between resectable and unresectable pancreatic cancers. Delftia is higher in resectable pancreatic cancer (Nakano et al. , 2022).

Reference：Nakano, S., Kawamoto, Y., Komatsu, Y., Saito, R., Ito, K., Yamamura, T., et al. (2022). Analysis of the pancreatic cancer microbiome using endoscopic ultrasound-guided fine-needle aspiration-derived samples. Pancreas 51, 351-357.DOI: 10.1097/MPA.0000000000002028

48.There was no significant difference in alpha diversity, beta diversity or taxonomic profiles between EUS-FNB and surgical resection Samples. (Masi et al., 2021)

References：Nakano, S., Kawamoto, Y., Komatsu, Y., Saito, R., Ito, K., Yamamura, T., et al. (2022). Analysis of the pancreatic cancer microbiome using endoscopic ultrasound-guided fine-needle aspiration-derived samples. Pancreas 51, 351-357. DOI: 10.1097/MPA.0000000000002028

Reference：Masi AC, Oppong YEA, Haugk B, Lamb CA, Sharp L, Shaw JM, Stewart CJ, Oppong KW. 2021.Endoscopic ultrasound (EUS)-guided fine needle biopsy (FNB) formalin fixed paraffin-embedded (FFPE) pancreatic tissue samples are a potential resource for microbiota analysis. *Gut* 70(5): 999-1001.  [DOI 10.1136/gutjnl-2020-322457](https://doi.org/10.1136/gutjnl-2020-322457)

49.***Bacteroides spp., Escherichia/Shigella spp., Acidaminococcus spp.*** which were predominant in pancreatic cyst fluids, while also a substantial ***Staphylococcus spp.*** and ***Fusobacterium spp.*** component was detected. (Li et al., 2017)

Reference：Li S, Fuhler GM, Bn N, Jose T, Bruno MJ, Peppelenbosch MP, Konstantinov SR. 2017. Pancreatic cyst fluid harbors a unique microbiome. Microbiome 5(1): 147. [DOI 10.1186/s40168-017-0363-6](https://doi.org/10.1186/s40168-017-0363-6)